

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/095,478

DATE: 06/17/98
TIME: 10:45:42

INPUT SET: S26785.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Plowman, Gregory

(ii) TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
PHOSPHATASE SuPTP05 AND
RELATED PRODUCTS AND
METHODS

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

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47 (B) FILING DATE:

48

49

50 (viii) ATTORNEY/AGENT INFORMATION:

51

52 (A) NAME: Warburg, Richard J.

53 (B) REGISTRATION NUMBER: 32,327

54 (C) REFERENCE/DOCKET NUMBER: 224/115

55

56

57 (ix) TELECOMMUNICATION INFORMATION:

58

59 (A) TELEPHONE: (213) 489-1600

60 (B) TELEFAX: (213) 955-0440

61 (C) TELEX: 67-3510

62

63

64

65 (2) INFORMATION FOR SEQ ID NO: 1:

66

67 (i) SEQUENCE CHARACTERISTICS:

68

69 (A) LENGTH: 426 amino acids

70 (B) TYPE: amino acid

71 (C) STRANDEDNESS: single

72 (D) TOPOLOGY: linear

73

74 (ii) MOLECULE TYPE: Peptide

75

76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

77

78 Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp

79 1 5 10 15

80

81 Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro

82 20 25 30

83

84 Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Ile Phe Gly Asn Lys

85 35 40 45

86

87 Met Asn Ser Glu Asn Val Lys Pro Ser His His Leu Ser Phe Ser Asp

88 50 55 60

89

90 Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu Ser Asp Thr Asp Glu

91 65 70 75 80

92

93 Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser

94 85 90 95

95

96 Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu

97 100 105 110

98

99 Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu

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100		115		120		125	
101							
102	Lys	Glu	Leu	Thr	Gln	Leu	Ala
103		130				135	
104							140
105	Ser	Ala	Arg	Ser	Ala	Met	Arg
106		145			150		155
107							160
108	Glu	Glu	Leu	Asp	Ile	Ile	Arg
109				165			170
110							175
111	Leu	Pro	Asp	Asp	Phe	Asn	Ser
112			180			185	
113							190
114	Asn	Arg	Tyr	Arg	Asp	Ile	Leu
115		195				200	
116							205
117	Gly	Lys	Asn	Lys	Asp	Tyr	Ile
118		210				215	
119							220
120	His	Glu	Glu	Glu	Tyr	Phe	Tyr
121		225			230		235
122							240
123	Thr	Ile	Glu	Asp	Phe	Trp	Gln
124				245			250
125							255
126	Ile	Ala	Met	Ile	Thr	Arg	Glu
127			260				265
128							270
129	Ser	Tyr	Trp	Pro	Ile	Ser	Leu
130		275				280	
131							285
132	Ser	Val	Phe	Leu	Glu	Thr	Phe
133		290				295	
134							300
135	Val	Phe	Gln	Ile	Val	Lys	Lys
136		305			310		315
137							320
138	His	Leu	Gln	Phe	Thr	Lys	Trp
139				325			330
140							335
141	Asp	Phe	Phe	Ile	Lys	Tyr	Val
142			340			345	
143							350
144	Gly	Pro	Leu	Leu	Val	His	Cys
145		355				360	
146							365
147	Phe	Ile	Cys	Val	Asp	Val	Val
148		370				375	
149							380
150	Phe	Asp	Ile	Met	Asn	Ile	Val
151		385			390		
152							395

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153 Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys Tyr Glu Ile Val Leu
154 405 410 415

155
156 Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr
157 420 425
158
159
160

161 (2) INFORMATION FOR SEQ ID NO: 2:
162

163 (i) SEQUENCE CHARACTERISTICS:
164

165 (A) LENGTH: 463 amino acids
166 (B) TYPE: amino acid
167 (C) STRANDEDNESS: single
168 (D) TOPOLOGY: linear
169

170 (ii) MOLECULE TYPE: Peptide
171

172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
173

174 Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
175 1 5 10 15
176

177 Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
178 20 25 30
179

180 Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Val Gln Asn Lys Asn
181 35 40 45
182

183 Leu Met Lys Tyr Glu Glu His Leu Asp Ile Leu Met Val Phe Leu Leu
184 50 55 60
185

186 Ile Lys Thr Ile Trp Tyr Asn Val Phe Lys Leu Trp Lys Gly Lys Leu
187 65 70 75 80
188

189 Ile Phe Gly Asn Lys Met Asn Ser Glu Asn Val Lys Pro Ser His His
190 85 90 95
191

192 Leu Ser Phe Ser Asp Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu
193 100 105 110
194

195 Ser Asp Thr Asp Glu Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg
196 115 120 125
197

198 Asn Arg Trp Asn Ser Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr
199 130 135 140
200

201 Val Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu
202 145 150 155 160
203

204 Thr Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro
205 165 170 175

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206
207   Leu Ile Phe Asn Ser Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn
208               180               185               190
209
210   Thr Leu Gln Lys Lys Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu
211               195               200               205
212
213   Leu Glu Gln Met Thr Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu
214               210               215               220
215
216   Gln Asn Arg Asp Lys Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser
217   225               230               235               240
218
219   Thr Arg Val Pro Leu Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr
220               245               250               255
221
222   Ile Arg Ile Val Asn His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln
223               260               265               270
224
225   Gly Pro Leu Pro Glu Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu
226               275               280               285
227
228   Asn Asn Cys Asn Val Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly
229   290               295               300
230
231   Val Ile Lys Cys Tyr Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu
232   305               310               315               320
233
234   Glu Phe Glu His Phe Ser Val Phe Leu Glu Thr Phe His Val Thr Gln
235               325               330               335
236
237   Tyr Phe Thr Val Arg Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys
238               340               345               350
239
240   Ser Gln Cys Val Lys His Leu Gln Phe Thr Lys Trp Pro Asp His Gly
241               355               360               365
242
243   Thr Pro Ala Ser Ala Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg
244               370               375               380
245
246   Lys Ser His Ile Thr Gly Pro Leu Leu Val His Cys Ser Ala Gly Val
247   385               390               395               400
248
249   Gly Arg Thr Gly Val Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile
250               405               410               415
251
252   Glu Lys Asn Tyr Ser Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg
253               420               425               430
254
255   Lys Gln Arg Cys Gly Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys
256               435               440               445
257
258   Tyr Glu Ile Val Leu Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text